



# Sequence Listing

<110> Ashkenazi, Avi J.  
Gurney, Austin

<120> RTD Receptor

<130> P1129R1 (REVISED)

<140> US 09/114,844

<141> 1998-07-14

<150> US 60/056,974

<151> 1997-08-26

<160> 10

<210> 1

<211> 386

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 310

<223> Xaa may be serine or leucine

<400> 1

Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg  
1 5 10 15

Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro  
20 25 30

Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val  
35 40 45

Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg  
50 55 60

Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg  
65 70 75

Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser  
80 85 90

Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr  
95 100 105

Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val  
110 115 120

Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg  
125 130 135

Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn  
140 145 150

Ser	Pro	Glu	Met	Cys	Arg	Thr	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	155	160	165
Met	Val	Lys	Val	Ser	Asn	Cys	Thr	Pro	Arg	Ser	Asp	Ile	Lys	Cys	170	175	180
Lys	Asn	Glu	Ser	Ala	Ala	Ser	Ser	Thr	Gly	Lys	Thr	Pro	Ala	Ala	185	190	195
Glu	Glu	Thr	Val	Thr	Thr	Ile	Leu	Gly	Met	Leu	Ala	Ser	Pro	Tyr	200	205	210
His	Tyr	Leu	Ile	Ile	Ile	Val	Val	Leu	Val	Ile	Ile	Leu	Ala	Val	215	220	225
Val	Val	Val	Gly	Phe	Ser	Cys	Arg	Lys	Lys	Phe	Ile	Ser	Tyr	Leu	230	235	240
Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Pro	Glu	Arg	Val	His	245	250	255
Arg	Val	Leu	Phe	Arg	Arg	Arg	Ser	Cys	Pro	Ser	Arg	Val	Pro	Gly	260	265	270
Ala	Glu	Asp	Asn	Ala	Arg	Asn	Glu	Thr	Leu	Ser	Asn	Arg	Tyr	Leu	275	280	285
Gln	Pro	Thr	Gln	Val	Ser	Glu	Gln	Glu	Ile	Gln	Gly	Gln	Glu	Leu	290	295	300
Ala	Glu	Leu	Thr	Gly	Val	Thr	Val	Glu	Xaa	Pro	Glu	Glu	Pro	Gln	305	310	315
Arg	Leu	Leu	Glu	Gln	Ala	Glu	Ala	Glu	Gly	Cys	Gln	Arg	Arg	Arg	320	325	330
Leu	Leu	Val	Pro	Val	Asn	Asp	Ala	Asp	Ser	Ala	Asp	Ile	Ser	Thr	335	340	345
Leu	Leu	Asp	Ala	Ser	Ala	Thr	Leu	Glu	Glu	Gly	His	Ala	Lys	Glu	350	355	360
Thr	Ile	Gln	Asp	Gln	Leu	Val	Gly	Ser	Glu	Lys	Leu	Phe	Tyr	Glu	365	370	375
Glu	Asp	Glu	Ala	Gly	Ser	Ala	Thr	Ser	Cys	Leu					380	385	

<210> 2

<211> 2082

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1085

<223> Y may be cytosine, thymine or uracil

<400> 2

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atccctcgac ctcgacccac gcgtccggaa cctttgcacg cgcacaaact 100

acggggacga tttctgattg atttttggcg ctttcgatcc accctcctcc 150

cttctc  atg gga ctt tgg gga caa agc gtc ccg acc gcc 189
        Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
          1             5             10

tcg agc gct cga gca ggg cgc tat cca gga gcc agg aca 228
Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr
          15             20

gcg tcg gga acc aga cca tgg ctc ctg gac ccc aag atc 267
Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile
  25             30             35

ctt aag ttc gtc gtc ttc atc gtc gcg gtt ctg ctg ccg 306
Leu Lys Phe Val Val Phe Ile Val Ala Val Leu Leu Pro
  40             45             50

gtc cgg gtt gac tct gcc acc atc ccc cgg cag gac gaa 345
Val Arg Val Asp Ser Ala Thr Ile Pro Arg Gln Asp Glu
          55             60

gtt ccc cag cag aca gtg gcc cca cag caa cag agg cgc 384
Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg Arg
  65             70             75

agc ctc aag gag gag gag tgt cca gca gga tct cat aga 423
Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg
          80             85

tca gaa tat act gga gcc tgt aac ccg tgc aca gag ggt 462
Ser Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
  90             95             100

gtg gat tac acc att gct tcc aac aat ttg cct tct tgc 501
Val Asp Tyr Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys
  105             110             115

ctg cta tgt aca gtt tgt aaa tca ggt caa aca aat aaa 540
Leu Leu Cys Thr Val Cys Lys Ser Gly Gln Thr Asn Lys
          120             125

agt tcc tgt acc acg acc aga gac acc gtg tgt cag tgt 579
Ser Ser Cys Thr Thr Thr Arg Asp Thr Val Cys Gln Cys
  130             135             140

gaa aaa gga agc ttc cag gat aaa aac tcc cct gag atg 618
Glu Lys Gly Ser Phe Gln Asp Lys Asn Ser Pro Glu Met
  145             150

tgc cgg acg tgt aga aca ggg tgt ccc aga ggg atg gtc 657
Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly Met Val
  155             160             165
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aag gtc agt aat tgt acg ccc cgg agt gac atc aag tgc 696  
Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys  
170 175 180

aaa aat gaa tca gct gcc agt tcc act ggg aaa acc cca 735  
Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro  
185 190

gca gcg gag gag aca gtg acc acc atc ctg ggg atg ctt 774  
Ala Ala Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu  
195 200 205

gcc tct ccc tat cac tac ctt atc atc ata gtg gtt tta 813  
Ala Ser Pro Tyr His Tyr Leu Ile Ile Ile Val Val Leu  
210 215

gtc atc att tta gct gtg gtt gtg gtt ggc ttt tca tgt 852  
Val Ile Ile Leu Ala Val Val Val Val Gly Phe Ser Cys  
220 225 230

cgg aag aaa ttc att tct tac ctc aaa ggc atc tgc tca 891  
Arg Lys Lys Phe Ile Ser Tyr Leu Lys Gly Ile Cys Ser  
235 240 245

ggt ggt gga gga ggt ccc gaa cgt gtg cac aga gtc ctt 930  
Gly Gly Gly Gly Gly Pro Glu Arg Val His Arg Val Leu  
250 255

ttc cgg cgg cgt tca tgt cct tca cga gtt cct ggg gcg 969  
Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly Ala  
260 265 270

gag gac aat gcc cgc aac gag acc ctg agt aac aga tac 1008  
Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr  
275 280

ttg cag ccc acc cag gtc tct gag cag gaa atc caa ggt 1047  
Leu Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly  
285 290 295

cag gag ctg gca gag cta aca ggt gtg act gta gag tyg 1086  
Gln Glu Leu Ala Glu Leu Thr Gly Val Thr Val Glu Xaa  
300 305 310

cca gag gag cca cag cgt ctg ctg gaa cag gca gaa gct 1125  
Pro Glu Glu Pro Gln Arg Leu Leu Glu Gln Ala Glu Ala  
315 320

gaa ggg tgt cag agg agg agg ctg ctg gtt cca gtg aat 1164  
Glu Gly Cys Gln Arg Arg Arg Leu Leu Val Pro Val Asn  
325 330 335

gac gct gac tcc gct gac atc agc acc ttg ctg gat gcc 1203  
Asp Ala Asp Ser Ala Asp Ile Ser Thr Leu Leu Asp Ala  
340 345

tcg gca aca ctg gaa gaa gga cat gca aag gaa aca att 1242  
 Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu Thr Ile  
 350 355 360

cag gac caa ctg gtg ggc tcc gaa aag ctc ttt tat gaa 1281  
 Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu  
 365 370 375

gaa gat gag gca ggc tct gct acg tcc tgc ctg tgaaag 1320  
 Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu  
 380 385

aatctcttca ggaaaccaga gcttccctca tttacctttt ctctacaaa 1370  
 gggaagcagc ctggaagaaa cagtccagta cttgacccat gcccacaaca 1420  
 actctactat ccaatatggg gcagcttacc aatggtccta gaactttggt 1470  
 aacgcacttg gagtaatttt tatgaaatac tgcgtgtgat aagcaaacgg 1520  
 gagaaattta tatcagattc ttggctgcat agttatacga ttgtgtatta 1570  
 agggtcgttt taggccacat gcggtggctc atgcctgtaa tcccagcact 1620  
 ttgataggct gaggcagggt gattgcttga gctcgggagt ttgagaccag 1670  
 cctcatcaac acagtgaaac tccatctcaa tttaaaaga aaaaaagtgg 1720  
 ttttaggatg tcattctttg cagttcttca tcatgagaca agtctttttt 1770  
 tctgcttctt atattgcaag ctccatctct actggtgtgt gcatttaatg 1820  
 acatctaact acagatgccg cacagccaca atgctttgcc ttatagtttt 1870  
 ttaactttag aacgggatta tcttgttatt acctgtattt tcagtttcgg 1920  
 atatttttga cttaatgatg agattatcaa gacgtacccc tatgctaagt 1970  
 catgagcata tggacttacg agggttcgac ttagagtttt gagctttaag 2020  
 ataggattat tgggggctta ccccccactt aattagaaga aacattttat 2070  
 attgctttac ta 2082

<210> 3

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> Sequence is synthesized.

<400> 3

cataaaagtt cctgcacat gaccagagac acagtgtgtc agtgtaaaga 50

<210> 4

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Sequence is synthesized.

<400> 4

cttcaggaaa ccagagcttc cctc 24

<210> 5

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Sequence is synthesized.

<400> 5

ttctcccgtt tgcttatcac acgc 24

<210> 6

<211> 191

<212> PRT

<213> Homo sapiens

<400> 6

Gly	Arg	Gly	Ala	Leu	Pro	Thr	Ser	Met	Gly	Gln	His	Gly	Pro	Ser
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Ala	Arg	Ala	Arg	Ala	Gly	Arg	Ala	Pro	Gly	Pro	Arg	Pro	Ala	Arg
				20					25					30

Glu	Ala	Ser	Pro	Arg	Leu	Arg	Val	His	Lys	Thr	Phe	Lys	Phe	Val
				35					40					45

Val	Val	Gly	Val	Leu	Leu	Gln	Val	Val	Pro	Ser	Ser	Ala	Ala	Thr
				50					55					60

Ile	Lys	Leu	His	Asp	Gln	Ser	Ile	Gly	Thr	Gln	Gln	Trp	Glu	His
				65					70					75

Ser	Pro	Leu	Gly	Glu	Leu	Cys	Pro	Pro	Gly	Ser	His	Arg	Ser	Glu
				80					85					90

Arg	Pro	Gly	Ala	Cys	Asn	Arg	Cys	Thr	Glu	Gly	Val	Gly	Tyr	Thr
				95					100					105

Asn	Ala	Ser	Asn	Asn	Leu	Phe	Ala	Cys	Leu	Pro	Cys	Thr	Ala	Cys
				110					115					120

Lys	Ser	Asp	Glu	Glu	Glu	Arg	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn
				125					130					135

Thr	Ala	Cys	Gln	Cys	Lys	Pro	Gly	Thr	Phe	Arg	Asn	Asp	Asn	Ser
				140					145					150

Ala	Glu	Met	Cys	Arg	Lys	Cys	Ser	Thr	Gly	Cys	Pro	Arg	Gly	Met
				155					160					165

Val Lys Val Lys Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val  
 170 175 180

His Lys Glu Ser Gly Asn Gly His Asn Ile Trp  
 185 190

<210> 7  
 <211> 193  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
 1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro  
 20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val  
 35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp  
 50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser  
 65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp  
 80 85 90

Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr  
 95 100 105

His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp  
 110 115 120

Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr  
 125 130 135

Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro  
 140 145 150

Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val  
 155 160 165

Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His  
 170 175 180

Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala  
 185 190

<210> 8  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<400> 8

Met	Ala	Arg	Ile	Pro	Lys	Thr	Leu	Lys	Phe	Val	Val	Val	Ile	Val
1				5					10					15
Ala	Val	Leu	Leu	Pro	Val	Leu	Ala	Tyr	Ser	Ala	Thr	Thr	Ala	Arg
				20					25					30
Gln	Glu	Glu	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg
				35					40					45
His	Ser	Phe	Lys	Gly	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	Ser
				50					55					60
Glu	His	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr
				65					70					75
Thr	Asn	Ala	Ser	Asn	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val
				80					85					90
Cys	Lys	Ser	Asp	Gln	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg
				95					100					105
Asp	Thr	Val	Cys	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn
				110					115					120
Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu
				125					130					135
Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val
				140					145					150
Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr							
				155										

<210> 9  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

Gly	Gly	Asp	Pro	Lys	Cys	Met	Asp	Arg	Val	Cys	Phe	Trp	Arg	Leu
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Gly	Leu	Leu	Arg	Gly	Pro	Gly	Ala	Glu	Asp	Asn	Ala	His	Asn	Glu
				20					25					30
Ile	Leu	Ser	Asn	Ala	Asp	Ser	Leu	Ser	Thr	Phe	Val	Ser	Glu	Gln
				35					40					45
Gln	Met	Glu	Ser	Gln	Glu	Pro	Ala	Asp	Leu	Thr	Gly	Val	Thr	Val
				50					55					60
Gln	Ser	Pro	Gly	Glu	Ala	Gln	Cys	Leu	Leu	Gly	Pro	Ala	Glu	Ala
				65					70					75
Glu	Gly	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	Gly	Ala
				80					85					90



Asp	Pro	Thr	Glu	Thr	Leu	Met	Leu	Phe	Phe	Asp	Lys	Phe	Ala	Asn
				95					100					105
Ile	Val	Pro	Phe	Asp	Ser	Trp	Asp	Gln	Leu	Met	Arg	Gln	Leu	Asp
				110					115					120
Leu	Thr	Lys	Asn	Glu	Ile	Asp	Val	Val	Arg	Ala	Gly	Thr	Ala	Gly
				125					130					135
Pro	Gly	Asp	Ala	Leu	Tyr	Ala	Met	Leu	Met	Lys	Trp	Val	Asn	Lys
				140					145					150
Thr	Gly	Arg	Asn	Ala	Ser	Ile	His	Thr	Leu	Leu	Asp	Ala	Leu	Glu
				155					160					165
Arg	Met	Glu	Glu	Arg	His	Ala	Lys	Glu	Lys	Ile	Gln	Asp	Leu	Leu
				170					175					180
Val	Asp	Ser	Gly	Lys	Phe	Ile	Tyr	Leu	Glu	Asp	Gly	Thr	Gly	Ser
				185					190					195
Ala	Val	Ser	Leu	Glu										
				200										

<210> 10  
 <211> 202  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Lys	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly
1				5					10					15
Asp	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu
				20					25					30
Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln
				35					40					45
Val	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr
				50					55					60
Gly	Val	Asn	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu
				65					70					75
Pro	Ala	Glu	Ala	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro
				80					85					90
Ala	Asn	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp
				95					100					105
Asp	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	Leu	Met
				110					115					120
Arg	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys	Val	Ala	Lys	Ala
				125					130					135

Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys  
140 145 150

Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu  
155 160 165

Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile  
170 175 180

Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly  
185 190 195

Asn Ala Asp Ser Ala Leu Ser  
200

C1  
cont